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sequences information comprising SEQ ID NOs:3502 to 7001 or function information based on the amino acid sequence is recorded,

said computer readable recording medium being optionally selected from the group consisting of a floppy disc, a hard disc, a magnetic tape, a random access memory (RAM), a read only memory (ROM), a magneto-optic disc (MO), CD-ROM, CD-R, CD-RW, DVD-ROM, DVD-RAM and DVD-RW.

REMARKS

Reconsideration and allowance in view of the foregoing amendment and the following remarks are respectfully requested.

Claims 69-110 are pending.

Responsive to the Office Action dated May 10, 2002, the applicants elect, with traverse, the subject matter of the Examiner's Group V for further prosecution in the above. The applicant's urge the Examiner to withdraw the restriction requirement and examine all the claimed subject matter. With specific regard to the requirement for election of a single sequence, the applicants urge the Examiner to appreciate that the subject matter of Group V relates to a method, a system and the like, using a database, nucleotide sequence of DNA's and amino acids sequences of proteins derived from a coryneform bacterium. The affects of the present invention and method of the presently claimed invention can be and are obtained therefore by using a number of sequences as the database. Methods to or using individual sequences such as the Examiner has suggested, may not provide complete protection for the applicants' disclosed invention and further would not likely serve as useful purpose to and for practicing the invention without the use of this full scope of the presently claimed invention. Clearly, in the invention of Group V, one nucleotide or amino acid sequence cannot be elected as a method to or involving such a single sequence is not believed to be appropriate. The

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applicants respectfully submit therefore, that all the nucleotide and amino acid sequences should be elected and made the subject of the Examiner's search.

The nature of the subject matter of Group V requires inclusion of more than one sequence and the Examiner is requested to reconsider and withdrawal the restriction requirement in this regard. The present response is submitted to be a bona fide and complete response to the Office Action of May 10, 2002. The Examiner is requested to contact the undersigned if anything further is required, however and allow additional time for providing any further response or comments which may be required.

An early and favorable Action on the merits is requested.

Respectfully submitted,

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IN THE CLAIMS

79. (Amended) A system based on a computer for identifying a target sequence or a target structure motif derived from a coryneform bacterium, which is optionally a microorganism of the genus *Corynebacterium*, the genus *Brevibacterium*, or the genus *Microbacterium*, and the microorganism belonging to the genus *Corynebacterium* is optionally selected from the group consisting of *Corynebacterium glutamicum*, *Corynebacterium acetoacidophilum*, *Corynebacterium acetoglutamicum*, *Corynebacterium callunae*, *Corynebacterium herculis*, *Corynebacterium lilium*, *Corynebacterium melassecola*, *Corynebacterium thermoaminogenes*, and *Corynebacterium ammoniagenes*, comprising the following:

- (i) a user input device that inputs [at least one nucleotide sequence information selected from] nucleotide sequences information comprising SEQ ID NOs:1 to 3501, or [at least one amino acid sequence information selected from] amino acid sequences information comprising SEQ ID NOs:3502 to 7001, and target sequence or target structure motif information;
- (ii) a data storage device for at least temporarily storing the input information;
- (iii) a comparator that compares the [at least one nucleotide sequence information selected from] nucleotide sequences information comprising SEQ ID NOs:1 to 3501 or the [at least one amino acid sequence information selected from] amino acid sequences information comprising SEQ ID NOs:3502 to 7001, with the target sequence or target structure motif information, recorded by the data storage device for screening and analyzing nucleotide sequence information which is coincident with or analogous to the target sequence or target structure motif information or for screening and analyzing

amino acid sequence information which is coincident with or analogous to the target sequence or target structure motif information; and

(iv) an output device that shows a screening or analyzing result obtained by the comparator.

80. (Amended) A method based on a computer for identifying a target sequence or a target structure motif derived from a coryneform bacterium, which is optionally a microorganism of the genus *Corynebacterium*, the genus *Brevibacterium*, or the genus *Microbacterium*, and the microorganism belonging to the genus *Corynebacterium* is optionally selected from the group consisting of *Corynebacterium glutamicum*, *Corynebacterium acetoacidophilum*, *Corynebacterium acetoglutamicum*, *Corynebacterium callunae*, *Corynebacterium herculis*, *Corynebacterium lilium*, *Corynebacterium melassecola*, *Corynebacterium thermoaminogenes*, and *Corynebacterium ammoniagenes*, comprising the following:

(i) inputting [at least one nucleotide sequence information selected from] nucleotide sequences information comprising SEQ ID NOs:1 to 3501, or [at least one amino acid sequence information selected from] amino acid sequences information comprising SEQ ID NOs:3502 to 7001, and the target sequence information or target structure motif information into a user input device;

(ii) at least temporarily storing said information;

(iii) comparing the [at least one nucleotide sequence information selected from] nucleotide sequences information comprising SEQ ID NOs:1 to 3501 with the target sequence or target structure motif information, or the [at least one amino acid sequence information selected from] amino acid sequences information comprising

SEQ ID NOs:3502 to 7001 with the target sequence or target structure motif information; and

(iv) screening and analyzing nucleotide sequence information which is coincident with or analogous to the target sequence or target structure motif information, or screening and analyzing amino acid sequence information which is coincident with or analogous to the target sequence or target structure motif information.

81. (Amended) A system based on a computer for determining a function of a polypeptide encoded by a polynucleotide having a target nucleotide sequence, or a polypeptide having a target amino acid sequence, derived from a coryneform bacterium, which is optionally a microorganism of the genus *Corynebacterium*, the genus *Brevibacterium*, or the genus *Microbacterium*, and the microorganism belonging to the genus *Corynebacterium* is optionally selected from the group consisting of *Corynebacterium glutamicum*, *Corynebacterium acetoacidophilum*, *Corynebacterium acetoglutamicum*, *Corynebacterium callunae*, *Corynebacterium herculis*, *Corynebacterium lilium*, *Corynebacterium melassecola*, *Corynebacterium thermoaminogenes*, and *Corynebacterium ammoniagenes*, comprising the following:

(i) a user input device that inputs [at least one nucleotide sequence information selected from] nucleotide sequences information comprising SEQ ID NOs:2 to 3501, function information of a polypeptide encoded by the nucleotide sequence, and target nucleotide sequence information, or [at least one amino acid sequence information selected from] amino acid sequences information comprising SEQ ID NOs:3502 to 7001, function information based on the amino acid sequence, and target amino acid sequence information;

(ii) a data storage device for at least temporarily storing the input information;

(iii) a comparator that compares the [at least one nucleotide sequence information selected from] nucleotide sequences information comprising SEQ ID NOs:2 to 3501 with the target nucleotide sequence information for determining a function of a polypeptide encoded by a polynucleotide having the target nucleotide sequence which is coincident with or analogous to the polynucleotide having [at least one nucleotide sequence information selected from] nucleotide sequences information comprising SEQ ID NOs:2 to 3501, or that compares the [at least one amino acid sequence information selected from] amino acid sequences information comprising SEQ ID NOs:3502 to 7001 with the target amino acid sequence information for determining a function of a polypeptide having the target amino acid sequence which is coincident with or analogous to the polypeptide having at least one amino acid sequence selected from SEQ ID NOs:3502 to 7001; and

(iv) an output devices that shows a function obtained by the comparator.

82. (Amended) A method based on a computer for determining a function of a polypeptide encoded by a polypeptide encoded by a polynucleotide having a target nucleotide sequence derived from a coryneform bacterium, which is optionally a microorganism of the genus *Corynebacterium*, the genus *Brevibacterium*, or the genus *Microbacterium*, and the microorganism belonging to the genus *Corynebacterium* is optionally selected from the group consisting of *Corynebacterium glutamicum*, *Corynebacterium acetoacidophilum*, *Corynebacterium acetoglutamicum*, *Corynebacterium callunae*, *Corynebacterium herculis*, *Corynebacterium lilium*, *Corynebacterium melassecola*, *Corynebacterium thermoaminogenes*, and *Corynebacterium ammoniagenes*, comprising the following:

(i) inputting [at least one nucleotide sequence information selected from] nucleotide sequences information comprising SEQ ID NOs:2 to 3501, function information of a polypeptide encoded by the nucleotide sequence, and target nucleotide sequence information, or [at least one amino acid sequence information selected from] amino acid sequences information comprising SEQ ID NOs:3502 to 7001, function information based on the amino acid sequence, and target amino acid sequence information;

(ii) at least temporarily storing said information;

(iii) comparing the [at least one nucleotide sequence information selected from] nucleotide sequences information comprising SEQ ID NOs:2 to 3501 with the target nucleotide sequence information, or comparing the [at least one amino acid sequence information selected from] amino acid sequences information comprising SEQ ID NOs:3502 to 7001 with the target amino acid sequence information; and

(iv) determining a function of a polypeptide encoded by a polynucleotide having the target nucleotide sequence which is coincident with or analogous to the polynucleotide having at least one nucleotide sequence selected from SEQ ID NOs:2 to 3501, or determining a function of a polypeptide having the target amino acid sequence which is coincident with or analogous to the polypeptide having at least one amino acid sequence selected from the SEQ ID NOs:3502 to 7001.

83. (Amended) A recording medium or storage device which is readable by a computer in which [at least one nucleotide sequence information selected from] nucleotide sequences information comprising SEQ ID NOs:1 to 3501 or function information based on the nucleotide sequence is recorded, or [at least one amino acid sequence information selected from] amino acid sequences information comprising

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